

SEQUENCE LISTING

<110> Ding, Jeak Ling
 Ho, Bow
 National University of Singapore

<120> Sushi Peptide Multimer

<130> 040184-000400US

<140> US 10/563,551
 <141> 2006-01-04

<150> CA 2,432,972
 <151> 2003-07-04

<150> WO PCT/SG04/00194
 <151> 2004-07-02

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<170> PatentIn Ver. 2.1

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 <213> Artificial Sequence

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 <223> Description of Artificial Sequence:synthetic
 34-mer Sushi-3 peptide (S3 peptide), residues
 268-301 of Factor C, Sushi3 domain, LPS-binding
 motif

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 1 5 10 15
 Phe Pro Gln Gly Thr Glu Val Thr Tyr Thr Cys Ser Gly Asn Tyr Phe
 20 25 30
 Leu Met

<210> 2
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 <223> Description of Artificial Sequence:synthetic
 34-mer Sushi-3delta peptide (S3delta peptide)

<400> 2
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 1 5 10 15
 Phe Pro Gln Gly Thr Glu Val Thr Tyr Thr Cys Ser Gly Asn Tyr Phe
 20 25 30
 Leu Met

<210> 3
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 <213> Artificial Sequence

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 <223> Description of Artificial Sequence:LPS-binding
 motif S3 PCR amplification forward primer

<400> 3
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 <213> Artificial Sequence

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 <223> Description of Artificial Sequence:LPS-binding
 motif S3 PCR amplification reverse primer

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 Val Leu Gly Leu Leu Ala Gln Lys Met Arg Pro Val Gln Ser Lys Gly
 15 20 25

gta gat cta ggc ttg tgt gat gaa acg agg ttc gag tgt aag tgt ggc 146
 Val Asp Leu Gly Leu Cys Asp Glu Thr Arg Phe Glu Cys Lys Cys Gly
 30 35 40

gat cca ggc tat gtg ttc aac att cca gtg aaa caa tgt aca tac ttt 194
 Asp Pro Gly Tyr Val Phe Asn Ile Pro Val Lys Gln Cys Thr Tyr Phe
 45 50 55

tat cga tgg agg ccg tat tgt aaa cca tgt gat gac ctg gag gct aag 242
 Tyr Arg Trp Arg Pro Tyr Cys Lys Pro Cys Asp Asp Leu Glu Ala Lys
 60 65 70 75

gat att tgt cca aag tac aaa cga tgt caa gag tgt aag gct ggt ctt	290
Asp Ile Cys Pro Lys Tyr Lys Arg Cys Gln Glu Cys Lys Ala Gly Leu	
80 85 90	
gat agt tgt gtt act tgt cca cct aac aaa tat ggt act tgg tgt agc	338
Asp Ser Cys Val Thr Cys Pro Pro Asn Lys Tyr Gly Thr Trp Cys Ser	
95 100 105	
ggt gaa tgt cag tgt aag aat gga ggt atc tgt gac cag agg aca gga	386
Gly Glu Cys Gln Cys Lys Asn Gly Gly Ile Cys Asp Gln Arg Thr Gly	
110 115 120	
gct tgt gca tgt cgt gac aga tat gaa ggg gtg cac tgt gaa att ctc	434
Ala Cys Ala Cys Arg Asp Arg Tyr Glu Gly Val His Cys Glu Ile Leu	
125 130 135	
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Lys Gly Cys Pro Leu Leu Pro Ser Asp Ser Gln Val Gln Glu Val Arg	
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Asn Pro Pro Asp Asn Pro Gln Thr Ile Asp Tyr Ser Cys Ser Pro Gly	
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Phe Lys Leu Lys Gly Met Ala Arg Ile Ser Cys Leu Pro Asn Gly Gln	
175 180 185	
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Trp Ser Asn Phe Pro Pro Lys Cys Ile Arg Glu Cys Ala Met Val Ser	
190 195 200	
tct cca gaa cat ggg aaa gtg aat gct ctt agt ggt gat atg ata gaa	674
Ser Pro Glu His Gly Lys Val Asn Ala Leu Ser Gly Asp Met Ile Glu	
205 210 215	
ggg gct act tta cgg ttc tca tgt gat agt ccc tac tac ttg att ggt	722
Gly Ala Thr Leu Arg Phe Ser Cys Asp Ser Pro Tyr Tyr Leu Ile Gly	
220 225 230 235	
caa gaa aca tta acc tgt cag ggt aat ggt cag tgg aat gga cag ata	770
Gln Glu Thr Leu Thr Cys Gln Gly Asn Gly Gln Trp Asn Gly Gln Ile	
240 245 250	
cca caa tgt aag aac ttg gtc ttc tgt cct gac ctg gat cct gta aac	818
Pro Gln Cys Lys Asn Leu Val Phe Cys Pro Asp Leu Asp Pro Val Asn	
255 260 265	
cat gct gaa cac aag gtt aaa att ggt gtg gaa caa aaa tat ggt cag	866
His Ala Glu His Lys Val Lys Ile Gly Val Glu Gln Lys Tyr Gly Gln	
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Phe Pro Gln Gly Thr Glu Val Thr Tyr Thr Cys Ser Gly Asn Tyr Phe	
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Leu Met Gly Phe Asp Thr Leu Lys Cys Asn Pro Asp Gly Ser Trp Ser	
300 305 310 315	

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Asp Ser Lys Ala Val Asp Phe Leu Asp Asp Val Gly Glu Pro Val Arg	
335 340 345	
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Ile His Cys Pro Ala Gly Cys Ser Leu Thr Ala Gly Thr Val Trp Gly	
350 355 360	
aca gcc ata tac cat gaa ctt tcc tca gtg tgt cgt gca gcc atc cat	1154
Thr Ala Ile Tyr His Glu Leu Ser Ser Val Cys Arg Ala Ala Ile His	
365 370 375	
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380 385 390 395	
ggc ccc tac tcg gac ttt ctg ggt agt gac ctg aat ggg ata aaa tcg	1250
Gly Pro Tyr Ser Asp Phe Leu Gly Ser Asp Leu Asn Gly Ile Lys Ser	
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gaa gag ttg aag tct ctt gcc cgg agt ttc cga ttc gat tat gtc cgt	1298
Glu Glu Leu Lys Ser Leu Ala Arg Ser Phe Arg Phe Asp Tyr Val Arg	
415 420 425	
tcc tcc aca gca ggt aaa tca gga tgt cct gat gga tgg ttt gag gta	1346
Ser Ser Thr Ala Gly Lys Ser Gly Cys Pro Asp Gly Trp Phe Glu Val	
430 435 440	
gac gag aac tgt gtg tac gtt aca tca aaa cag aga gcc tgg gaa aga	1394
Asp Glu Asn Cys Val Tyr Val Thr Ser Lys Gln Arg Ala Trp Glu Arg	
445 450 455	
gct caa ggt gtg tgt acc aat atg gct gct cgt ctt gct gtg ctg gac	1442
Ala Gln Gly Val Cys Thr Asn Met Ala Ala Arg Leu Ala Val Leu Asp	
460 465 470 475	
aaa gat gta att cca aat tcg ttg act gag act cta cga ggg aaa ggg	1490
Lys Asp Val Ile Pro Asn Ser Leu Thr Glu Thr Leu Arg Gly Lys Gly	
480 485 490	
tta aca acc acg tgg ata gga ttg cac aga cta gat gct gag aag ccc	1538
Leu Thr Thr Thr Trp Ile Gly Leu His Arg Leu Asp Ala Glu Lys Pro	
495 500 505	
ttt att tgg gag tta atg gat cgt agt aat gtg gtt ctg aat gat aac	1586
Phe Ile Trp Glu Leu Met Asp Arg Ser Asn Val Val Leu Asn Asp Asn	
510 515 520	
cta aca ttc tgg gcc tct ggc gaa cct gga aat gaa act aac tgt gta	1634
Leu Thr Phe Trp Ala Ser Gly Glu Pro Gly Asn Glu Thr Asn Cys Val	
525 530 535	
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Tyr Met Asp Ile Gln Asp Gln Leu Gln Ser Val Trp Lys Thr Lys Ser	
540 545 550 555	

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Cys Phe Gln Pro Ser Phe Ala Cys Met Met Asp Leu Ser Asp Arg	
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Asn Lys Ala Lys Cys Asp Asp Pro Gly Ser Leu Glu Asn Gly His Ala	
575 580 585	
aca ctt cat gga caa agt att gat ggg ttc tat gct ggt tct tct ata	1826
Thr Leu His Gly Gln Ser Ile Asp Gly Phe Tyr Ala Gly Ser Ser Ile	
590 595 600	
agg tac agc tgt gag gtt ctc cac tac ctc agt gga act gaa acc gta	1874
Arg Tyr Ser Cys Glu Val Leu His Tyr Leu Ser Gly Thr Glu Thr Val	
605 610 615	
act tgt aca aca aat ggc aca tgg agt gct cct aaa cct cga tgt atc	1922
Thr Cys Thr Thr Asn Gly Thr Trp Ser Ala Pro Lys Pro Arg Cys Ile	
620 625 630 635	
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Lys Val Ile Thr Cys Gln Asn Pro Pro Val Pro Ser Tyr Gly Ser Val	
640 645 650	
gaa atc aaa ccc cca agt cgg aca aac tcg ata agt cgt gtt ggg tca	2018
Glu Ile Lys Pro Pro Ser Arg Thr Asn Ser Ile Ser Arg Val Gly Ser	
655 660 665	
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Pro Phe Leu Arg Leu Pro Arg Leu Pro Leu Pro Leu Ala Arg Ala Ala	
670 675 680	
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Lys Pro Pro Pro Lys Pro Arg Ser Ser Gln Pro Ser Thr Val Asp Leu	
685 690 695	
gct tct aaa gtt aaa cta cct gaa ggt cat tac cgg gta ggg tct cga	2162
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700 705 710 715	
gcc atc tac acg tgc gag tcg aga tac tac gaa cta ctt gga tct caa	2210
Ala Ile Tyr Thr Cys Glu Ser Arg Tyr Tyr Glu Leu Leu Gly Ser Gln	
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Ile Ser Arg Trp Leu Ala Asp His Asn Met Trp Phe Leu Gln Cys Gly	
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Thr Tyr Ser Ala Thr Ala Glu Ile Ile Asp Pro Asn Gln Phe Lys Met	
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Gln Val Arg Glu Ala Leu Glu Ile His Val Asn Pro Asn Tyr Asp Pro	
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880 885 890	
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cta cct gtt gtt gca gcc agc acc tgt gaa gag ggg tac aag gaa gca	2834
Leu Pro Val Val Ala Ala Ser Thr Cys Glu Glu Gly Tyr Lys Glu Ala	
925 930 935	
gac tta cca ctg aca gta aca gag aac atg ttc tgt gca ggt tac aag	2882
Asp Leu Pro Leu Thr Val Thr Glu Asn Met Phe Cys Ala Gly Tyr Lys	
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Lys Gly Arg Tyr Asp Ala Cys Ser Gly Asp Ser Gly Gly Pro Leu Val	
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Phe Ala Asp Asp Ser Arg Thr Glu Arg Arg Trp Val Leu Glu Gly Ile	
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Gly Phe Thr Lys Val Asn Val Phe Leu Ser Trp Ile Arg Gln Phe Ile	
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<212> PRT

<213> Carinoscorpius rotundicauda

<220>

<223> Factor C

<400> 6

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Cys	Asp	Glu	Thr	Arg	Phe	Glu	Cys	Lys	Cys	Gly	Asp	Pro	Gly	Tyr	Val	35	40	45	
Phe	Asn	Ile	Pro	Val	Lys	Gln	Cys	Thr	Tyr	Phe	Tyr	Arg	Trp	Arg	Pro	50	55	60	
Tyr	Cys	Lys	Pro	Cys	Asp	Leu	Glu	Ala	Lys	Asp	Ile	Cys	Pro	Lys		65	70	75	80
Tyr	Lys	Arg	Cys	Gln	Glu	Cys	Lys	Ala	Gly	Leu	Asp	Ser	Cys	Val	Thr	85	90		95
Cys	Pro	Pro	Asn	Lys	Tyr	Gly	Thr	Trp	Cys	Ser	Gly	Glu	Cys	Gln	Cys	100	105	110	
Lys	Asn	Gly	Gly	Ile	Cys	Asp	Gln	Arg	Thr	Gly	Ala	Cys	Ala	Cys	Arg	115	120	125	
Asp	Arg	Tyr	Glu	Gly	Val	His	Cys	Glu	Ile	Leu	Lys	Gly	Cys	Pro	Leu	130	135	140	
Leu	Pro	Ser	Asp	Ser	Gln	Val	Gln	Glu	Val	Arg	Asn	Pro	Pro	Asp	Asn	145	150	155	160
Pro	Gln	Thr	Ile	Asp	Tyr	Ser	Cys	Ser	Pro	Gly	Phe	Lys	Leu	Lys	Gly	165	170	175	
Met	Ala	Arg	Ile	Ser	Cys	Leu	Pro	Asn	Gly	Gln	Trp	Ser	Asn	Phe	Pro	180	185	190	
Pro	Lys	Cys	Ile	Arg	Glu	Cys	Ala	Met	Val	Ser	Ser	Pro	Glu	His	Gly	195	200	205	
Lys	Val	Asn	Ala	Leu	Ser	Gly	Asp	Met	Ile	Glu	Gly	Ala	Thr	Leu	Arg	210	215	220	
Phe	Ser	Cys	Asp	Ser	Pro	Tyr	Tyr	Leu	Ile	Gly	Gln	Glu	Thr	Leu	Thr	225	230	235	240
Cys	Gln	Gly	Asn	Gly	Gln	Trp	Asn	Gly	Gln	Ile	Pro	Gln	Cys	Lys	Asn	245	250	255	
Leu	Val	Phe	Cys	Pro	Asp	Leu	Asp	Pro	Val	Asn	His	Ala	Glu	His	Lys	260	265	270	
Val	Lys	Ile	Gly	Val	Glu	Gln	Lys	Tyr	Gly	Gln	Phe	Pro	Gln	Gly	Thr	275	280	285	
Glu	Val	Thr	Tyr	Thr	Cys	Ser	Gly	Asn	Tyr	Phe	Leu	Met	Gly	Phe	Asp	290	295	300	
Thr	Leu	Lys	Cys	Asn	Pro	Asp	Gly	Ser	Trp	Ser	Gly	Ser	Gln	Pro	Ser	305	310	315	320

Cys	Val	Lys	Val	Ala	Asp	Arg	Glu	Val	Asp	Cys	Asp	Ser	Lys	Ala	Val	325	330	335
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Gly	Cys	Ser	Leu	Thr	Ala	Gly	Thr	Val	Trp	Gly	Thr	Ala	Ile	Tyr	His	355	360	365
Glu	Leu	Ser	Ser	Val	Cys	Arg	Ala	Ala	Ile	His	Ala	Gly	Lys	Leu	Pro	370	375	380
Asn	Ser	Gly	Gly	Ala	Val	His	Val	Val	Asn	Asn	Gly	Pro	Tyr	Ser	Asp	385	390	400
Phe	Leu	Gly	Ser	Asp	Leu	Asn	Gly	Ile	Lys	Ser	Glu	Glu	Leu	Lys	Ser	405	410	415
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Lys	Ser	Gly	Cys	Pro	Asp	Gly	Trp	Phe	Glu	Val	Asp	Glu	Asn	Cys	Val	435	440	445
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Thr	Asn	Met	Ala	Ala	Arg	Leu	Ala	Val	Leu	Asp	Lys	Asp	Val	Ile	Pro	465	470	475
Asn	Ser	Leu	Thr	Glu	Thr	Leu	Arg	Gly	Lys	Gly	Leu	Thr	Thr	Thr	Trp	485	490	495
Ile	Gly	Leu	His	Arg	Leu	Asp	Ala	Glu	Lys	Pro	Phe	Ile	Trp	Glu	Leu	500	505	510
Met	Asp	Arg	Ser	Asn	Val	Val	Leu	Asn	Asp	Asn	Leu	Thr	Phe	Trp	Ala	515	520	525
Ser	Gly	Glu	Pro	Gly	Asn	Glu	Thr	Asn	Cys	Val	Tyr	Met	Asp	Ile	Gln	530	535	540
Asp	Gln	Leu	Gln	Ser	Val	Trp	Lys	Thr	Lys	Ser	Cys	Phe	Gln	Pro	Ser	545	550	555
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Ser	Ile	Asp	Gly	Phe	Tyr	Ala	Gly	Ser	Ser	Ile	Arg	Tyr	Ser	Cys	Glu	595	600	605
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Ser	Arg	Thr	Asn	Ser	Ile	Ser	Arg	Val	Gly	Ser	Pro	Phe	Leu	Arg	Leu	660	665	670
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Pro	Arg	Ser	Ser	Gln	Pro	Ser	Thr	Val	Asp	Leu	Ala	Ser	Lys	Val	Lys	690	695	700
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Glu	Ser	Arg	Tyr	Tyr	Glu	Leu	Leu	Gly	Ser	Gln	Gly	Arg	Arg	Cys	Asp	725	730	735
Ser	Asn	Gly	Asn	Trp	Ser	Gly	Arg	Pro	Ala	Ser	Cys	Ile	Pro	Val	Cys	740	745	750
Gly	Arg	Ser	Asp	Ser	Pro	Arg	Ser	Pro	Phe	Ile	Trp	Asn	Gly	Asn	Ser	755	760	765
Thr	Glu	Ile	Gly	Gln	Trp	Pro	Trp	Gln	Ala	Gly	Ile	Ser	Arg	Trp	Leu	770	775	780
Ala	Asp	His	Asn	Met	Trp	Phe	Leu	Gln	Cys	Gly	Gly	Ser	Leu	Leu	Asn	785	790	795
																		800


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Ala Glu Ile Ile Asp Pro Asn Gln Phe Lys Met Tyr Leu Gly Lys Tyr
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Leu Glu Ile His Val Asn Pro Asn Tyr Asp Pro Gly Asn Leu Asn Phe
      850      855      860
Asp Ile Ala Leu Ile Gln Leu Lys Thr Pro Val Thr Leu Thr Thr Arg
      865      870      875      880
Val Gln Pro Ile Cys Leu Pro Thr Asp Ile Thr Thr Arg Glu His Leu
      885      890      895
Lys Glu Gly Thr Leu Ala Val Val Thr Gly Trp Gly Leu Asn Glu Asn
      900      905      910
Asn Thr Tyr Ser Glu Thr Ile Gln Gln Ala Val Leu Pro Val Val Ala
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Ala Ser Thr Cys Glu Glu Gly Tyr Lys Glu Ala Asp Leu Pro Leu Thr
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Val Thr Glu Asn Met Phe Cys Ala Gly Tyr Lys Lys Gly Arg Tyr Asp
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Ala Cys Ser Gly Asp Ser Gly Gly Pro Leu Val Phe Ala Asp Asp Ser
      965      970      975
Arg Thr Glu Arg Arg Trp Val Leu Glu Gly Ile Val Ser Trp Gly Ser
      980      985      990
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<210> 7

<211> 36

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:recombinant S3
monomer (rS3-1mer) peptide, with additional Pro
and Asp at ends from acid cleavage of rS3-4mer DP
linker

<400> 7

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<210> 8

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<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:recombinant S3
tetramer (rS3-4mer) tandem repeat peptide with
acid cleavable DP linker between S3 units

<220>

<221> CDS

<222> (1)..(468)

<223> rS3-4mer

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Pro Gln Asp Pro His Ala Glu His Lys Val Lys Ile Gly Val Glu Gln	
1 5 10 15	
aaa tat ggt cag ttt cct caa ggc act gaa gtg acc tat acg tgt tcg	96
Lys Tyr Gly Gln Phe Pro Gln Gly Thr Glu Val Thr Tyr Thr Cys Ser	
20 25 30	
ggt aac tac ttc ttg atg gac ccc cag gat ccc cat gct gaa cac aag	144
Gly Asn Tyr Phe Leu Met Asp Pro Gln Asp Pro His Ala Glu His Lys	
35 40 45	
gtt aaa att ggt gtg gaa caa aaa tat ggt cag ttt cct caa ggc act	192
Val Lys Ile Gly Val Glu Gln Lys Tyr Gly Gln Phe Pro Gln Gly Thr	
50 55 60	
gaa gtg acc tat acg tgt tcg ggt aac tac ttc ttg atg gac ccc cag	240
Glu Val Thr Tyr Thr Cys Ser Gly Asn Tyr Phe Leu Met Asp Pro Gln	
65 70 75 80	
gat ccc cat gct gaa cac aag gtt aaa att ggt gtg gaa caa aaa tat	288
Asp Pro His Ala Glu His Lys Val Lys Ile Gly Val Glu Gln Lys Tyr	
85 90 95	
ggt cag ttt cct caa ggc act gaa gtg acc tat acg tgt tcg ggt aac	336
Gly Gln Phe Pro Gln Gly Thr Glu Val Thr Tyr Thr Cys Ser Gly Asn	
100 105 110	
tac ttc ttg atg gac ccc cag gat ccc cat gct gaa cac aag gtt aaa	384
Tyr Phe Leu Met Asp Pro Gln Asp Pro His Ala Glu His Lys Val Lys	
115 120 125	
att ggt gtg gaa caa aaa tat ggt cag ttt cct caa ggc act gaa gtg	432
Ile Gly Val Glu Gln Lys Tyr Gly Gln Phe Pro Gln Gly Thr Glu Val	
130 135 140	
acc tat acg tgt tcg ggt aac tac ttc ttg atg gac	468
Thr Tyr Thr Cys Ser Gly Asn Tyr Phe Leu Met Asp	
145 150 155	

<210> 9

<211> 156

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:recombinant S3
tetramer (rS3-4mer) tandem repeat peptide with
acid cleavable DP linker between S3 units

<400> 9

Pro Gln Asp Pro His Ala Glu His Lys Val Lys Ile Gly Val Glu Gln
 1 5 10 15

Lys Tyr Gly Gln Phe Pro Gln Gly Thr Glu Val Thr Tyr Thr Cys Ser
 20 25 30

Gly Asn Tyr Phe Leu Met Asp Pro Gln Asp Pro His Ala Glu His Lys
 35 40 45

Val Lys Ile Gly Val Glu Gln Lys Tyr Gly Gln Phe Pro Gln Gly Thr
 50 55 60

Glu Val Thr Tyr Thr Cys Ser Gly Asn Tyr Phe Leu Met Asp Pro Gln
 65 70 75 80

Asp Pro His Ala Glu His Lys Val Lys Ile Gly Val Glu Gln Lys Tyr
 85 90 95

Gly Gln Phe Pro Gln Gly Thr Glu Val Thr Tyr Thr Cys Ser Gly Asn
 100 105 110

Tyr Phe Leu Met Asp Pro Gln Asp Pro His Ala Glu His Lys Val Lys
 115 120 125

Ile Gly Val Glu Gln Lys Tyr Gly Gln Phe Pro Gln Gly Thr Glu Val
 130 135 140

Thr Tyr Thr Cys Ser Gly Asn Tyr Phe Leu Met Asp
 145 150 155

<210> 10

<211> 4

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:amino acids
 used to link S3 multimer to remainder of
 polypeptide

<400> 10

Ile Glu Gly Arg
 1

<210> 11

<211> 7

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:enterokinase
 recognition sequence, enterokinase cleavage site

<220>

<221> MOD_RES

<222> (1)..(7)

<223> Xaa = any amino acid

<220>

<221> MOD_RES

<222> (4)..(5)

<223> Asp at positions 4 and 5 may be present or absent

<400> 11

Xaa Asp Asp Asp Asp Lys Xaa

1

5